

SEQUENCE LISTING

<110> Helix Research Institute

<120> NOVEL GENES ASSOCIATED WITH THE MAINTENANCE
OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS

<130> H1-107PCT1

<140>

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<150> JP 1999-248036

<151> 1999-07-29

<150> JP 2000-118776

<151> 2000-01-11

<150> JP 2000-183767

<151> 2000-05-02

<150> US 60/159590

<151> 1999-10-18

<150> US 60/183322

<151> 2000-02-17

1053549-01300

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Ins
AI

130

.140

Phe Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala

145

150

155

Arg Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala

160

165

170

175

Lys Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln

180

185

190

His Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu

195

200

205

Val Cys Asn Ala Ala Thr Phe Ala Leu ~~Pro~~ Trp Ser Leu Thr Lys Asp

210

215

220

Gly Leu Glu Thr Thr Phe Gln Val Asn His ~~Leu~~ Gly His Phe Tyr Leu

225

230

235

Ins
AI

Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser

340

345

350

atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa 1225

Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu

355

360

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ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg 1273

Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met

370

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ccc tca cca gaa gct cag agc gaa gag acg gcc cgg acc ctg tgg gcg 1321

Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala

385

390

395

ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc 1366

Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

400

405

410

taagtggagc tcagagcgga tgggcacaca caccgcct gtgtgtgtcc cctcagcaa 1426

gtgccagggc tgggcccctt ccaaagtcc ctcaaaca gatccgcaag agtaaaggaa 1486

ataagagcag tcacaacaga gtgaaaaatc ttaagtacca atgggaagca gggaattcct 1546

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40059519-01202

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tggcctgttt gaaagtaaaa acctgcttgg tgtgtaggtt ccgtatctcc ctggagaagc 1666
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2026-07-19
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<210> 2

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8/19

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Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu Asp

1 5 10 15

Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp Val

20 25 30

Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys

35 40 45

Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu

50 55 60

Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn

65 70 75 80

Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp

85 90 95

Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr

100 105 110

Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val

40265519-012303
Ins
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115 120 125
 Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe
 130 135 140
 Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg
 145 150 155 160
 Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys
 165 170 175
 Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His
 180 185 190
 Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val
 195 200 205
 Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly
 210 215 220
 Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val
 225 230 235 240
 Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile
 245 250 255

10059919-01293
 200210-0355001

Ins
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10/19

Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu

260

265

270

Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp

275

280

285

Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser

290

295

300

Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala

305

310

315

320

Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp

325

330

335

Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met

340

345

350

Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu

355

360

365

Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro

370

375

380

Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala Leu

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203240655004
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Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly

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<211> 251

<212> DNA

<213> Gallus gallus

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<221> CDS

<222> (3).. (251)

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Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu

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gaa gaa aaa aca cag tgg gaa cat cca aaa tct ggg aag agg aaa cgt 95

Glu Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg

20

25

30

gtt gca gga ggt ctg cca tat gga tgg gag cag gag act gat gaa aat 143

Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn

35

40

45

203210255001
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gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg 191
 Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu
 50 55 60

gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct 239
 Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro
 65 70 75

act aga caa aaa 251
 Thr Arg Gln Lys
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<210> 4

<211> 83

<212> PRT

<213> Gallus gallus

<400> 4

Glu Arg Thr Thr Lys Asp Gly Trp Val Tyr Tyr Ala Asn His Leu Glu
 1 5 10 15

Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg Val
 20 25 30

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35 40 45

50 55 60

65 70 \ 75 80

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
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<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<212> DNA

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<212> DNA

<213> Artificial Sequence

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4056649-04299

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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